

Fractal Shape of Cancer Tumor Growth

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Abstract

Nanobacteria possess unusual properties, making their detection difficult with standard microbiological methods. Scientists are interested in nanoparticles, their origin, activity, and biological toxicity. The large number of publications on nanomaterials is in a wide range of fields, including chemistry, physics, materials engineering, biology, medicine, and electronics. Very small particles, so-called nanoparticles, have the ability to damage living organisms. This ability results primarily from their small size, which allows them to penetrate and travel within the circulatory systems of a host. We inhale them with every breath, and consume them with every drink. Nanobacteria play an important role in many chronic diseases where infectious pathogens have not been suspected.

In this study, we have shown nanobacteria capable of acting as crystallization centers for the formation of cluster structures. At high concentrations, nanoparticles tend to cluster, forming aggregates. Nanoparticles usually form atmospheric fractal-like dendritic aggregates.

We have simulated the nanobacteria growth based on epidemic model by Monte Carlo method. The result figures are fractal. We have compared these figures with brain and womb cancer tumor images. Fractal dimension has been found out by box counting method. Calculation of fractal dimension shows the same dimension for simulation results and cancer tumors for scales $100 < R < 1000$. It means that we can categorize cancer tumors in regard of their statistical properties such as fractal dimension. Nanoparticles are generally classified based on their dimensionality, morphology, composition, uniformity, and agglomeration. There are significant common fractal aspects between our simulation results and cancer tumor images.

Keywords

Fracta; Dimension; Simulation; Tumor; Mont Carlo; Cancer

Introduction

Growth processes are nonequilibrium and it can occur in nature and technology. Some examples include electrodeposition [Matsushita M., 1984], viscous fingering [Måløy K. J., 1985], nanobacteria colonies [Matsushita M., 1990], ecological or metabolic networks [Bastolla, U., 2009- Guimerà, 2005], phase transition theory and correlation functions [Cavagna,

A., 2010 - Vicsek, T., 1995] and neuritis formation [Caserta F., 1990]. Computer models for simulation of the growth of clusters, generally constituted by identical particles, are used for the understanding of aggregation phenomena. These models investigate the underlying physical rules and the properties observed in growth phenomena. One of the exceptional characteristics of fractals is that they can be described by a non integer dimension. The most interesting features of the fractal structures found in nature and computer models, is scale invariance which can be found without fine-tuning of any parameter, in contrast with usual critical phenomena that scale invariance only emerges at a critical point [Stanley H. E., 1971].

The best example of nonequilibrium growth model is the diffusion-limited aggregation (DLA) model introduced by Witten and Sander in 1981 [Witten T. A., 1981] in which the particles do not follow Brownian trajectories until they touch and stick in an aggregate. The DLA model leads to very complex aggregates with multiscale properties [Amitrano C. 1991 - Mandelbrot B. B., 2002] and multifractality in the growth-site probability distribution [Amitrano C. 1986 - Sander L. M., 2000]. If the random walks in the DLA model are replaced by ballistic trajectories at random directions, it is named as the ballistic aggregation (BA) model proposed by Vold [Vold M. J., 1963 - Meakin P., 1998]. Differently from DLA, the BA model has non-fractal clusters characterized by a power law [Liang S., 1985 - Vicsek T., 1992]. The third standard model was proposed by Eden [Eden M., 1961- Eden M., 1958] as a basic model for the biological pattern formation for instance, tumor growth and nanobacteria colonies. In this model, new particles are added to the empty neighborhood of the cluster without overlap with previously aggregated particles [Wang C. Y., 1995- Ferreira S. C., 2006]. The DLA, BA, and Eden models can be simulated by constraining the particle positions to the sites of an underlying lattice. It is well known that lattice anisotropy has strong effects on the cluster shape and scaling [Goold N. R., 2005- Zabolitzky J. G. 1986- Batchelor M. J., 1991].

Biological organisms are regarded as typical examples

of complex systems, and such populations are supposed to behave in complex ways. Therefore we investigated colony formation in nanobacteria cluster, which is described as being some of the simplest biological organism. The use of statistical physics to solve biological problems has yielded novel result. During the last twenty years, Matsuyama et al. [Matsuyama, T., 1989] and Fujikawa and Matsushita [Fujikawa, H., 1989] showed that nanobacteria colony patterns obtained in the laboratory can be fractal objects [Barabási, A.-L. 1995]. Both experimental and theoretical investigations have shown a clear picture of the different structures that such colonies can exhibit.

In this paper, we have used Epidemic model to simulate nanobacteria growth and have measured the fractal dimension of nanobacteria colonies. We will find fractal dimension of cancer tumors which, is the same as fractal dimension of simulation results.

Model

In the context of the spread of disease, one usually wants to know the conditions for an epidemic. A simple lattice model of the spread of a disease (Epidemic model) can be formulated as follows. Suppose that an occupied site corresponds to an infected person. Initially there is a single infected person and the four nearest neighbor sites (on the square lattice) correspond to susceptible people. At the next time step, we visit the four susceptible sites and occupy (infect) each site with probability p . If a susceptible site is not occupied, we say that the site is immune and we do not test it again. We then find the new susceptible sites and continue until either the disease is controlled or reaches the boundary of the lattice. This growth model of a disease generates a cluster of infected sites with probability p [Harvey Gould, 2006]. The results are well known as a fractal. The discussed simple epidemic model generates the same clusters as in the percolation model [Sahimi Muhamm, 1994].

We chose a seed site at the center of the lattice for simplicity. The unoccupied nearest neighbors of the occupied sites (four sites) are growth sites. In the simplest version of the model, a growth site is chosen at random and occupied. The newly occupied site is removed from the list of growth sites and the new growth sites are added to the list. This process is repeated many times until a large cluster of occupied sites is formed (FIG. 1) [Harvey Gould, 2006].

Although the model is unrealistic from the biological point of view, it produces compact aggregates with a nontrivial interface scaling usually analyzed through the interface width w . Intensive numerical simulations indicate a power-law growth of the interface width with the time, $w \sim t^\beta$, and exponent $\beta = 1/3$ [Vicsek T., 1992-Ferreira S. C., 2006 -Kertész J. 1988-Devillard P., 1989], corresponding to the Kardar-Parisi-Zhang (KPZ) universality class [Kardar M., 1986]. The results are well known as a fractal.

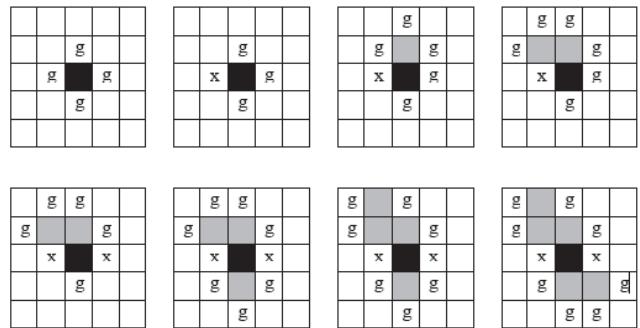


FIG. 1 AN EXAMPLE OF THE GROWTH OF A PERCOLATION CLUSTER. SITES ARE OCCUPIED WITH PROBABILITY p . OCCUPIED SITES ARE REPRESENTED BY A SHADED SQUARE, GROWTH SITES ARE LABELED BY G, AND TESTED UNOCCUPIED SITES ARE LABELED BY X. BECAUSE THE SEED SITE IS OCCUPIED BUT NOT TESTED, WE HAVE REPRESENTED IT DIFFERENTLY THAN THE OTHER OCCUPIED SITES. THE GROWTH SITES ARE CHOSEN AT RANDOM [HARVEY GOULD, 2006]

One of the most common methods for calculating the fractal dimension of a self-similar fractal is the box counting method. Consider a line of length L broken up into segments of length r (FIG. 2a). The number of segments or "boxes", N , which is needed to cover the line is related to the size r of the box by [Rubin H., 2008]:

$$N(r) = \frac{L}{r} = \frac{C}{r} \quad (1)$$

where C is a constant. A proposed definition of fractional dimension is the power of r in this expression as $r \rightarrow 0$. In this example, the line has dimension $df = 1$. In order to know how many little circles of radius r it would take to cover or fill a circle of area A (FIG. 2b), we will find that

$$N(r) = \lim_{r \rightarrow 0} \frac{A}{\pi r^2} \Rightarrow d_f = 2 \quad (2)$$

as expected. Likewise, counting the number of little spheres or cubes that can be packed within a large sphere tells us that a sphere has dimension $df = 3$. In general, if it takes N little spheres or cubes of side $r \rightarrow 0$

to cover some object, then the fractal dimension df can be deduced

$$N(r) = C \left(\frac{L}{r} \right)^{df} = CS^{df} \quad (as \quad r \rightarrow 0) \quad (3)$$

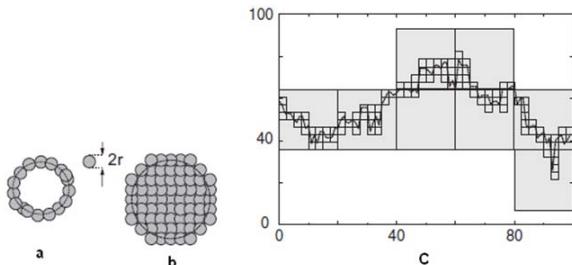


FIG. 2 EXAMPLES OF THE USE OF BOX COUNTING TO DETERMINE FRACTAL DIMENSION. A)- THE PERIMETER IS BEING COVERED, IN THE B)- AN ENTIRE FIG. IS BEING COVERED, AND ON THE C)- A "COASTLINE" IS BEING COVERED BY BOXES OF TWO DIFFERENT SIZES (SCALES)

$$\log N(r) = \log C - d_f \log(r) \quad (r \rightarrow 0),$$

$$\Rightarrow d_f = -\lim_{r \rightarrow 0} \frac{\Delta N(r)}{\Delta r} \quad (4)$$

Here $s \propto 1/r$ is called the scale in geography, so $r \rightarrow 0$ corresponds to an infinite scale. FIG. 2c shows a "coastline" is being covered by boxes of two different sizes (scales) as an example. We have used box counting to determine the fractal dimension which means a value for df [Rubin H., 2008].

Result and Discussion

Using straightforward Monte Carlo methods, we have simulated a square lattice 100×100 based on Epidemic model which has been shown in FIG. 1. The initial seed is base on time and probability has been changed from $p=0.1$ to $p=0.9$. It has been repeated 10 times for each p then averaged. The results with probability $p=0.32$ and $p=0.42$ have been illustrated in FIG. 3 and 4 respectively with random seed based on time. The result FIG.s. are well known as a fractal.

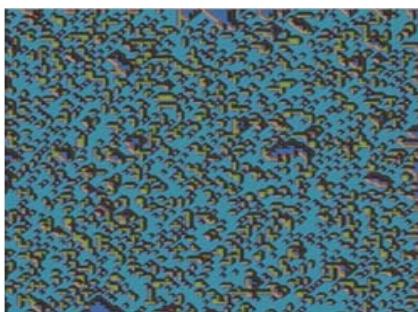


FIG. 3 SIMULATION RESULT WITH P=0.32 AND RANDOM SEED BASED ON TIME

In order to find fractal dimension, we have used box counting method. FIG. 5a is the linear behavior of the number of box as a function of the size of box for FIG. 3. The red dashed line shows the expected scaling for a space-filling 2D image. The discrepancy between the two curves indicates a possible fractal behavior.

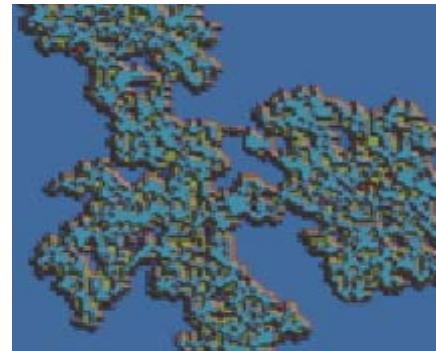


FIG. 4 SIMULATION RESULT WITH P=0.42 AND RANDOM SEED BASED ON TIME

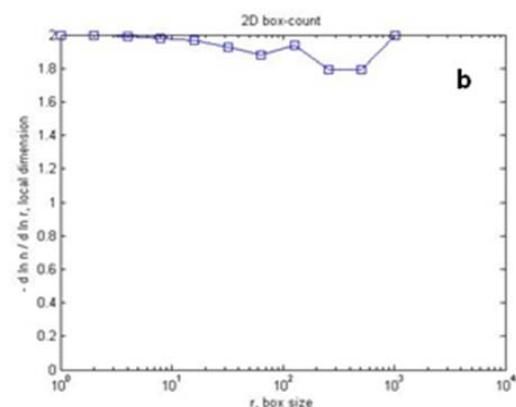
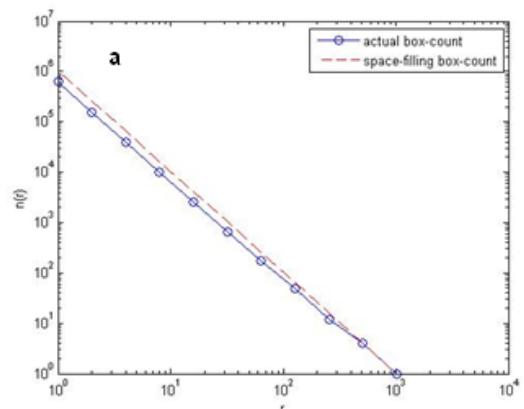


FIG. 5 A) THE SLOPE OF THE DASHED LINE IS EQUAL TO THE SLOPE OF THE DATA. B) LOGARITHMIC PLOT OF THE DATA CORRESPONDING TO THE SIMULATION OF FIG. 3. THE SLOPE OF THE GRAPH IS EXPECTED TO APPROACHED TO 1.8 FOR SCALES $100 < R < 1000$. IN THIS REGION THE SLOPE OF THE DATA CORRESPONDS TO THE FRACTAL DIMENSION

Fractal dimension of FIG. 3 has been calculated. The local slope shows that the image is indeed fractal, with

a fractal dimension for scales $100 < R < 1000$ (FIG. 5b).

The same box counting method has been done for the data of FIG. 4 and results have been shown in FIG s. 6a and 6b. As it can be seen that the fractal dimension for two data sets are the same. We have done it for 10 data sets result of 10 simulation with different probability $p=0.1$ to $p=0.9$ and random seed. The fractal dimensions are the same.

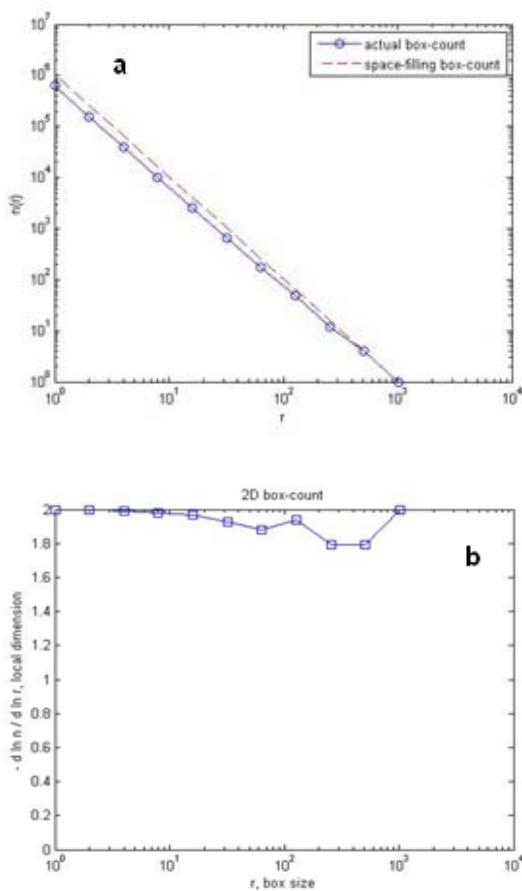


FIG. 6 A) THE SLOPE OF THE DASHED LINE IS EQUAL TO THE SLOPE OF THE DATA. B) LOGARITHMIC PLOT OF THE DATA CORRESPONDING TO THE SIMULATION OF FIG. 4. THE SLOPE OF THE GRAPH IS EXPECTED TO APPROACHED TO 1.8 FOR SCALES $100 < R < 1000$. IN THIS REGION THE SLOPE OF THE DATA CORRESPONDS TO THE FRACTAL DIMENSION

Fractals arise from a variety of sources and have been observed in nature and on computer simulations. The geometry of fractals and the mathematics of fractal dimension have provided useful tools for a variety of scientific subjects, among of which is cancer tumor growth which is the growth on nanobacteria. In order to compare this fractal dimension with cancer, we have chosen some images of tumor growth and have calculated fractal dimension of them by box counting method. The calculation of fractal dimension for about 10 tumors shows the same amount ~ 1.8 for all of them.

FIG. 7 shows the image of lung cancer tumor. The result of box counting method has been shown in FIGs. 8a and 8b.

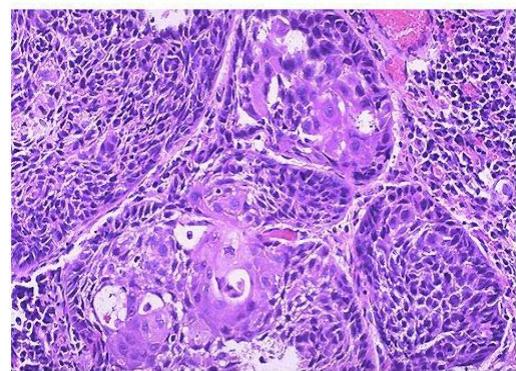


FIG 7: THE IMAGE OF LUNG CANCER TUMOR

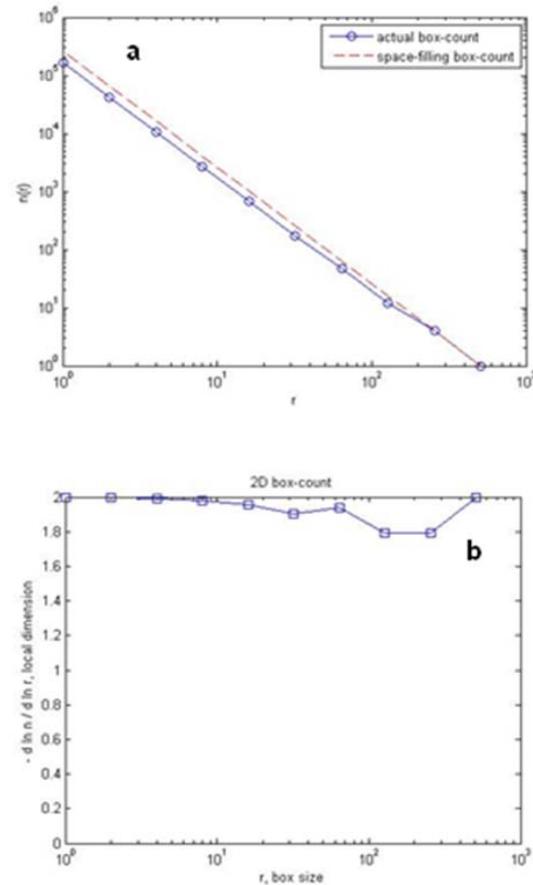


FIG. 8 A) THE SLOPE OF THE DASHED LINE IS EQUAL TO THE SLOPE OF THE DATA. B) LOGARITHMIC PLOT OF THE DATA CORRESPONDING TO THE SIMULATION OF FIG. 7. THE SLOPE OF THE GRAPH IS EXPECTED TO APPROACHED TO 1.8 FOR SCALES $100 < R < 1000$. IN THIS REGION THE SLOPE OF THE DATA CORRESPONDS TO THE FRACTAL DIMENSION

FIG. 9 demonstrates the tumor of liver and FIG s. 10a and 10b are fractal dimension of FIG. 9 which is about 1.8. All results of simulation and tumor images are consistent.

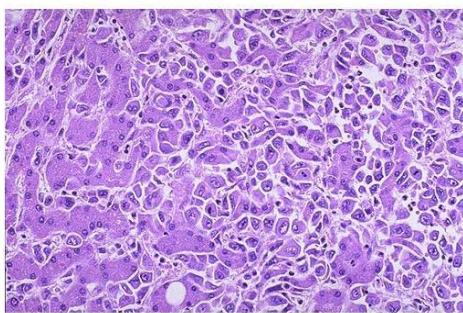


FIG 9: THE IMAGE OF LIVER CANCER TUMOR

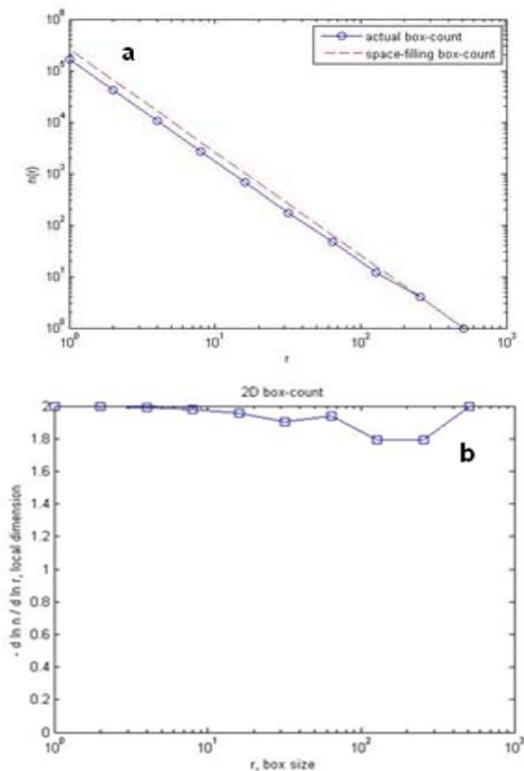


FIG. 10 A) THE SLOPE OF THE DASHED LINE IS EQUAL TO THE SLOPE OF THE DATA. B) LOGARITHMIC PLOT OF THE DATA CORRESPONDING TO THE SIMULATION OF FIG. 9. THE SLOPE OF THE GRAPH IS EXPECTED TO APPROACHED TO 1.8 FOR SCALES $100 < R < 1000$. IN THIS REGION THE SLOPE OF THE DATA CORRESPONDS TO THE FRACTAL DIMENSION

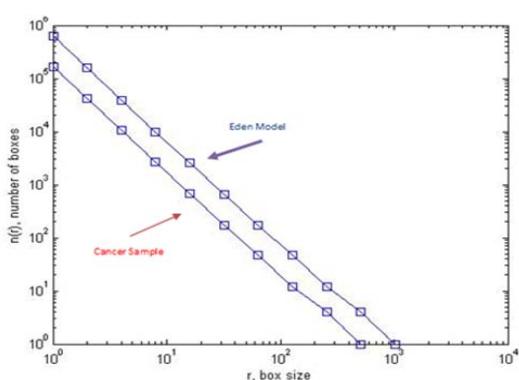


FIG 11 COMPARISON OF FRACTAL DIMENSION OF SIMULATION RESULT AND CANCER IMAGE

In FIG 11 we have compared two fractal dimension due to simulation and real cancer image. The slope of two line is the same which, means fractal dimension is the same.

Conclusion

The statistical investigation has been developed in many fields of physics. In this view, we can get some information different with medical knowledge. Classification of cancer tumors based on fractal dimension helps us to find a new method to study cancer without having details. We tested it for 10 cancer cases. But it is needed to check with more cases. It would be possible to know in this way, how dangerous are the cancer tumors. There is in need to find more cancer cases to compare and categorize. In summary, we have introduced a new class of cluster growth models which are characterized by simulation of a finite lattice growth sites. Of course to find an applicable method, it needs more research. There is an outlook to improve this study.

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